Supplemental Table 3: PMCA results for SNPs at the 2q24.3 locus using the 20-way alignments of mammals, reproduced from Claussnitzer et al. 2014. Sall summary statistic as in Claussnitzer et al 2014. TFiMrestr, number of TF motifs in restricted modules (>50% conservation); TFiM, transcription factor motifs in all modules; TF, number of TF motifs conserved across >50% of species regardless of modules; Modules, number of TF modules total

SNP	**LD (r2)**	**LD (D')**	**chromosome**	**position**	**A1**	**A2**				**AF**	**WTFBS**	**p-estTFBS**	**Wmodules**	**p-estmodules**	**WTFBS_in_modul**	**p-estTFBS_in_ mo**	**Sall**	**Wrestr-TFBS**	**p-estrestr-TFBS**	**Wrestr-modules**	**p-estrestr-module**	**Wrestr-TFBS_in_m**	**p-estrestr-TFBS_i**	**Srestr-all**
rs10195252	0.84	0.99	chr2	164656581	T	C	0.79	0.29	0.1	0.42	38	0.004	14347	0.000998	185	0.000998	8.4	17	0.000998	12	0.000998	14	0.000998	9
rs10187501	0.9	0.96	chr2	164675944	A	G	0.71	0.27	0.08	0.38	122	0.019	68577	0.000998	549	0.000998	7.72	37	0.000998	114	0.000998	61	0.000998	9
rs6753142	0.87	0.95	chr2	164687561	T	C	0.74	0.27	0.11	0.39	53	0.000998	61330	0.000998	356	0.000998	9	21	0.000998	1332	0.000998	107	0.000998	9
rs6712203	0.82	0.94	chr2	164700808	C	T	0.76	0.28	0.11	0.4	460	0.000999	140577	0.000998	1716	0.000998	9	312	0.000998	32402	0.000998	763	0.000998	9
rs10179126	0.95	0.98	chr2	164655284	C	G	0.76	0.28	0.1	0.38	43	0.0549	632	0.000998	89	0.000998	7.26	15	0.00999	2	0.000998	3	0.000999	8
rs2198550	0.84	0.92	chr2	164700250	A	C	0.71	0.28	0.08	0.38	104	0.22	63018	0.000998	364	0.011	5.62	56	0.164	188	0.000998	72	0.003	6.31
rs6752978	0.84	0.92	chr2	164696432	G	T	0.72	0.27	0.08	0.38	59	0.393	54199	0.000998	251	0.00699	5.56	28	0.253	15	0.005	18	0.00699	5.05
rs7592412	0.91	0.97	chr2	164669828	T	C	0.76	0.28	0.1	0.38	270	0.158	128218	0.000998	847	0.000998	6.8	77	0.131	6	0.00799	9	0.031	4.49
rs12692737	0.84	0.92	chr2	164697799	C	A	0.71	0.27	0.08	0.38	138	0.179	77617	0.000998	502	0.000998	6.75	38	0.212	2	0.0949	3	0.0979	2.71
rs12692735	0.96	0.99	chr2	164648055	G	T	0.76	0.28	0.1	0.39	27	0.491	3514	0.000998	131	0.002	6.01	8	0.503	1	0.103	2	0.103	2.27
rs10930133	0.97	0.99	chr2	164650214	T	A	0.76	0.28	0.1	0.39	104	0.353	56405	0.000998	417	0.000998	6.45	24	0.426	1	0.175	2	0.175	1.89
rs6713419	0.97	0.99	chr2	164651790	T	C	0.76	0.29	0.1	0.39	79	0.113	57172	0.000998	338	0.000998	6.95	22	0.043	0	1	0	1	1.37
rs13432797	0.9	0.97	chr2	164670077	G	C	0.71	0.27	0.09	0.37	96	0.551	1249	0.000998	136	0.042	4.64	42	0.45	1	0.312	2	0.312	1.36
rs36105243	0.91	0.97	chr2	164668241	C	G	0.76	0.28	0.09	0.38	98	0.24	95152	0.000998	547	0.000998	6.62	7	0.0809	0	1	0	1	1.09
rs3923113	1	1	chr2	164645339	A	C	0.76	0.29	0.12	0.38	98	0.24	95152	0.000998	547	0.000998	6.62	7	0.0809	0	1	0	1	1.09
rs10184004	0.85	0.99	chr2	164651879	C	T	0.79	0.3	0.1	0.42	70	0.02	81827	0.000998	406	0.000998	7.7	8	0.0889	0	1	0	1	1.05
rs6738627	0.87	0.95	chr2	164687940	G	A	0.76	0.28	0.11	0.39	100	0.244	48266	0.000998	321	0.000999	6.61	11	0.192	0	1	0	1	0.717
rs6754919	0.97	0.99	chr2	164651333	C	T	0.76	0.28	0.1	0.39	56	0.413	1664	0.000998	130	0.00599	5.61	14	0.24	0	1	0	1	0.62
rs7609045	0.84	0.92	chr2	164698697	G	A	0.71	0.27	0.08	0.38	104	0.283	50311	0.000998	386	0.00699	5.7	7	0.386	0	1	0	1	0.414
rs9653282	0.83	0.92	chr2	164698148	A	T	0.71	0.27	0.08	0.39	108	0.629	99245	0.000998	521	0.00599	5.42	14	0.629	0	1	0	1	0.201